

SEQUENCE LISTING

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MOSSAKOWSKA, Danuta, Ewa, Irena

<120> CONJUGATES OF SOLUBLE PEPTIDIC COMPOUNDS WITH
MEMBRANE-BINDING AGENTS

<130> 37945-0004

<140> US 09/612,314
<141> 2000-07-07

<150> US 09/214,913
<151> 1999-03-16

<150> PCT/EP97/03715
<151> 1997-07-08

<150> GB 96 148 71.3
<151> 1996-07-15

<160> 67

<170> PatentIn Ver. 2.1

<210> 1
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.2

<400> 1
gcaccgcagt gcatcatccc gaacaaatgc taataaa 37

<210> 2
<211> 37
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.1

<400> 2
agctttttatt agcatttggtt cgggatgatg cactgcg 37

<210> 3
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:

Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.4 to generate fragment 4

<400> 3
gcaccgcagt gcacatccc gaacaaagac ggtccgaaaa agaagaaaaa gaaatctccg 60
tccaaatctt ccggttgcta ataaa 85

<210> 4
<211> 85
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used to anneal to oligonucleotide
of SEQ ID NO.3 to generate fragment 4

<400> 4
agcttttatt agcaaccgga agatttggac ggagatttct ttttcttctt tttcggaccg 60
tctttgttcg ggatgatgca ctgcg 85

<210> 5
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (17)
<223> NH2 group is linked to the C-terminal cysteine

<220>
<223> Description of Artificial Sequence: Peptide used
to synthesie MSWP-1

<400> 5
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 6
<211> 198
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: The petide
sequence correpsonds to short consensus repeats
1-3 of CR1 with a C-terminal cysteine

<400> 6
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Cys
195

<210> 7
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Short
consensus repeats 1-3 of CR1 with an additional 17
C-terminal amino acids

<400> 7
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro
 195 200 205
 Ser Lys Ser Ser Gly Cys
 210

<210> 8
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (198)..(199)
 <223> Residues 1-198 are a first polypeptide chain and
 residues 199-215 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (215)
 <223> The C-terminal glycine is linked to an
 N-(Myristoyl) group

<220>
 <221> UNSURE
 <222> (198)
 <223> The cysteine at position 198 is -Cys-COOH

<220>
 <221> UNSURE
 <222> (199)
 <223> The cysteine at position 199 is CONH2-Cys-

<220>
 <223> Description of Artificial Sequence:
 [SCR1-3]-Cys-S-S-[MSWP-1]

<400> 8
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

<220>
 <223> Description of Artificial Sequence: [SCR1-3/switch
 fusion] disulphide linked to [MSWP-1]

<220>
 <221> UNSURE
 <222> (214)
 <223> The cysteine at position 214 is -Cys-COOH

<220>
 <221> UNSURE
 <222> (215)
 <223> The cysteine at position 215 is CONH2-Cys-

<400> 9
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15
 Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30
 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45
 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60
 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro
 195 200 205
 Ser Lys Ser Ser Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
 210 215 220
 Ser Pro Ser Lys Ser Ser Gly
 225 230

<210> 10
 <211> 1947
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1930)..(1931)
 <223> Residues 1-1930 are a first polypeptide chain and
 residues 1931-1947 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 1930 and 1931

<220>
 <221> UNSURE
 <222> (1947)
 <223> The C-terminal glycine is linked to an
 N-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence: [CR1: 1-1929]
 - Cys-S-S-[MSWP-1]

<220>
 <221> UNSURE
 <222> (1930)
 <223> The cysteine at position 1930 is -Cys-COOH

<220>
 <221> UNSURE
 <222> (1931)
 <223> The Cysteine at position 1931 is CONH2-Cys-

<400> 10
 Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn Leu
 1 5 10 15
 Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu Cys
 20 25 30
 Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys Asn
 35 40 45
 Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys Arg
 50 55 60
 Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly Ile
 65 70 75 80
 Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg Leu
 85 90 95
 Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val Ile
 100 105 110
 Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu Pro
 115 120 125
 Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn Phe
 130 135 140

His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly Gly
 145 150 155 160
 Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr Ser
 165 170 175
 Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys Ile
 180 185 190
 Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn Gly Ile Leu Val
 195 200 205
 Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val Val Glu Phe Arg
 210 215 220
 Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg Val Lys Cys Gln
 225 230 235 240
 Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys Ser Arg Val Cys
 245 250 255
 Gln Pro Pro Pro Asp Val Leu His Ala Glu Arg Thr Gln Arg Asp Lys
 260 265 270
 Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser Cys Glu Pro Gly
 275 280 285
 Tyr Asp Leu Arg Gly Ala Ala Ser Met Arg Cys Thr Pro Gln Gly Asp
 290 295 300
 Trp Ser Pro Ala Ala Pro Thr Cys Glu Val Lys Ser Cys Asp Asp Phe
 305 310 315 320
 Met Gly Gln Leu Leu Asn Gly Arg Val Leu Phe Pro Val Asn Leu Gln
 325 330 335
 Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln Leu Lys
 340 345 350
 Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser Leu Trp
 355 360 365
 Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser Pro Pro
 370 375 380
 Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val Phe Pro
 385 390 395 400
 Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp Arg Gly
 405 410 415
 Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr Ser Asp
 420 425 430
 Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys Gly Ile
 435 440 445
 Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys Leu Lys
 450 455 460

Thr	Gln	Thr	Asn	Ala	Ser	Asp	Phe	Pro	Ile	Gly	Thr	Ser	Leu	Lys	Tyr	465	470	475	480
Glu	Cys	Arg	Pro	Glu	Tyr	Tyr	Gly	Arg	Pro	Phe	Ser	Ile	Thr	Cys	Leu	485	490	495	
Asp	Asn	Leu	Val	Trp	Ser	Ser	Pro	Lys	Asp	Val	Cys	Lys	Arg	Lys	Ser	500	505	510	
Cys	Lys	Thr	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Thr	515	520	525	
Asp	Ile	Gln	Val	Gly	Ser	Arg	Ile	Asn	Tyr	Ser	Cys	Thr	Thr	Gly	His	530	535	540	
Arg	Leu	Ile	Gly	His	Ser	Ser	Ala	Glu	Cys	Ile	Leu	Ser	Gly	Asn	Ala	545	550	555	560
Ala	His	Trp	Ser	Thr	Lys	Pro	Pro	Ile	Cys	Gln	Arg	Ile	Pro	Cys	Gly	565	570	575	
Leu	Pro	Pro	Thr	Ile	Ala	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	580	585	590	
Asn	Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	595	600	605	
Gly	Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	610	615	620	
Thr	Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	625	630	635	640
Cys	Ile	Ile	Pro	Asn	Lys	Cys	Thr	Pro	Pro	Asn	Val	Glu	Asn	Gly	Ile	645	650	655	
Leu	Val	Ser	Asp	Asn	Arg	Ser	Leu	Phe	Ser	Leu	Asn	Glu	Val	Val	Glu	660	665	670	
Phe	Arg	Cys	Gln	Pro	Gly	Phe	Val	Met	Lys	Gly	Pro	Arg	Arg	Val	Lys	675	680	685	
Cys	Gln	Ala	Leu	Asn	Lys	Trp	Glu	Pro	Glu	Leu	Pro	Ser	Cys	Ser	Arg	690	695	700	
Val	Cys	Gln	Pro	Pro	Pro	Asp	Val	Leu	His	Ala	Glu	Arg	Thr	Gln	Arg	705	710	715	720
Asp	Lys	Asp	Asn	Phe	Ser	Pro	Gly	Gln	Glu	Val	Phe	Tyr	Ser	Cys	Glu	725	730	735	
Pro	Gly	Tyr	Asp	Leu	Arg	Gly	Ala	Ala	Ser	Met	Arg	Cys	Thr	Pro	Gln	740	745	750	
Gly	Asp	Trp	Ser	Pro	Ala	Ala	Pro	Thr	Cys	Glu	Val	Lys	Ser	Cys	Asp	755	760	765	
Asp	Phe	Met	Gly	Gln	Leu	Leu	Asn	Gly	Arg	Val	Leu	Phe	Pro	Val	Asn	770	775	780	

Leu Gln Leu Gly Ala Lys Val Asp Phe Val Cys Asp Glu Gly Phe Gln
 785 790 795 800
 Leu Lys Gly Ser Ser Ala Ser Tyr Cys Val Leu Ala Gly Met Glu Ser
 805 810 815
 Leu Trp Asn Ser Ser Val Pro Val Cys Glu Gln Ile Phe Cys Pro Ser
 820 825 830
 Pro Pro Val Ile Pro Asn Gly Arg His Thr Gly Lys Pro Leu Glu Val
 835 840 845
 Phe Pro Phe Gly Lys Ala Val Asn Tyr Thr Cys Asp Pro His Pro Asp
 850 855 860
 Arg Gly Thr Ser Phe Asp Leu Ile Gly Glu Ser Thr Ile Arg Cys Thr
 865 870 875 880
 Ser Asp Pro Gln Gly Asn Gly Val Trp Ser Ser Pro Ala Pro Arg Cys
 885 890 895
 Gly Ile Leu Gly His Cys Gln Ala Pro Asp His Phe Leu Phe Ala Lys
 900 905 910
 Leu Lys Thr Gln Thr Asn Ala Ser Asp Phe Pro Ile Gly Thr Ser Leu
 915 920 925
 Lys Tyr Glu Cys Arg Pro Glu Tyr Tyr Gly Arg Pro Phe Ser Ile Thr
 930 935 940
 Cys Leu Asp Asn Leu Val Trp Ser Ser Pro Lys Asp Val Cys Lys Arg
 945 950 955 960
 Lys Ser Cys Lys Thr Pro Pro Asp Pro Val Asn Gly Met Val His Val
 965 970 975
 Ile Thr Asp Ile Gln Val Gly Ser Arg Ile Asn Tyr Ser Cys Thr Thr
 980 985 990
 Gly His Arg Leu Ile Gly His Ser Ser Ala Glu Cys Ile Leu Ser Gly
 995 1000 1005
 Asn Thr Ala His Trp Ser Thr Lys Pro Pro Ile Cys Gln Arg Ile Pro
 1010 1015 1020
 Cys Gly Leu Pro Pro Thr Ile Ala Asn Gly Asp Phe Ile Ser Thr Asn
 1025 1030 1035 1040
 Arg Glu Asn Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Leu
 1045 1050 1055
 Gly Ser Arg Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile
 1060 1065 1070
 Tyr Cys Thr Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala
 1075 1080 1085
 Pro Gln Cys Ile Ile Pro Asn Lys Cys Thr Pro Pro Asn Val Glu Asn
 1090 1095 1100

Gly Ile Leu Val Ser Asp Asn Arg Ser Leu Phe Ser Leu Asn Glu Val
 1105 1110 1115 1120
 Val Glu Phe Arg Cys Gln Pro Gly Phe Val Met Lys Gly Pro Arg Arg
 1125 1130 1135
 Val Lys Cys Gln Ala Leu Asn Lys Trp Glu Pro Glu Leu Pro Ser Cys
 1140 1145 1150
 Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu His Gly Glu His Thr
 1155 1160 1165
 Pro Ser His Gln Asp Asn Phe Ser Pro Gly Gln Glu Val Phe Tyr Ser
 1170 1175 1180
 Cys Glu Pro Gly Tyr Asp Leu Arg Gly Ala Ala Ser Leu His Cys Thr
 1185 1190 1195 1200
 Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg Cys Ala Val Lys Ser
 1205 1210 1215
 Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly Arg Val Leu Phe Pro
 1220 1225 1230
 Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe Val Cys Asp Glu Gly
 1235 1240 1245
 Phe Arg Leu Lys Gly Ser Ser Val Ser His Cys Val Leu Val Gly Met
 1250 1255 1260
 Arg Ser Leu Trp Asn Asn Ser Val Pro Val Cys Glu His Ile Phe Cys
 1265 1270 1275 1280
 Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His Thr Gly Thr Pro Ser
 1285 1290 1295
 Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr Thr Cys Asp Pro His
 1300 1305 1310
 Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly Glu Ser Thr Ile Arg
 1315 1320 1325
 Cys Thr Ser Asp Pro His Gly Asn Gly Val Trp Ser Ser Pro Ala Pro
 1330 1335 1340
 Arg Cys Glu Leu Ser Val Arg Ala Gly His Cys Lys Thr Pro Glu Gln
 1345 1350 1355 1360
 Phe Pro Phe Ala Ser Pro Thr Ile Pro Ile Asn Asp Phe Glu Phe Pro
 1365 1370 1375
 Val Gly Thr Ser Leu Asn Tyr Glu Cys Arg Pro Gly Tyr Phe Gly Lys
 1380 1385 1390
 Met Phe Ser Ile Ser Cys Leu Glu Asn Leu Val Trp Ser Ser Val Glu
 1395 1400 1405
 Asp Asn Cys Arg Arg Lys Ser Cys Gly Pro Pro Pro Glu Pro Phe Asn
 1410 1415 1420

Gly Met Val His Ile Asn Thr Asp Thr Gln Phe Gly Ser Thr Val Asn
 1425 1430 1435 1440
 Tyr Ser Cys Asn Glu Gly Phe Arg Leu Ile Gly Ser Pro Ser Thr Thr
 1445 1450 1455
 Cys Leu Val Ser Gly Asn Asn Val Thr Trp Asp Lys Lys Ala Pro Ile
 1460 1465 1470
 Cys Glu Ile Ile Ser Cys Glu Pro Pro Pro Thr Ile Ser Asn Gly Asp
 1475 1480 1485
 Phe Tyr Ser Asn Asn Arg Thr Ser Phe His Asn Gly Thr Val Val Thr
 1490 1495 1500
 Tyr Gln Cys His Thr Gly Pro Asp Gly Glu Gln Leu Phe Glu Leu Val
 1505 1510 1515 1520
 Gly Glu Arg Ser Ile Tyr Cys Thr Ser Lys Asp Asp Gln Val Gly Val
 1525 1530 1535
 Trp Ser Ser Pro Pro Pro Arg Cys Ile Ser Thr Asn Lys Cys Thr Ala
 1540 1545 1550
 Pro Glu Val Glu Asn Ala Ile Arg Val Pro Gly Asn Arg Ser Phe Phe
 1555 1560 1565
 Ser Leu Thr Glu Ile Ile Arg Phe Arg Cys Gln Pro Gly Phe Val Met
 1570 1575 1580
 Val Gly Ser His Thr Val Gln Cys Gln Thr Asn Gly Arg Trp Gly Pro
 1585 1590 1595 1600
 Lys Leu Pro His Cys Ser Arg Val Cys Gln Pro Pro Pro Glu Ile Leu
 1605 1610 1615
 His Gly Glu His Thr Leu Ser His Gln Asp Asn Phe Ser Pro Gly Gln
 1620 1625 1630
 Glu Val Phe Tyr Ser Cys Glu Pro Ser Tyr Asp Leu Arg Gly Ala Ala
 1635 1640 1645
 Ser Leu His Cys Thr Pro Gln Gly Asp Trp Ser Pro Glu Ala Pro Arg
 1650 1655 1660
 Cys Thr Val Lys Ser Cys Asp Asp Phe Leu Gly Gln Leu Pro His Gly
 1665 1670 1675 1680
 Arg Val Leu Leu Pro Leu Asn Leu Gln Leu Gly Ala Lys Val Ser Phe
 1685 1690 1695
 Val Cys Asp Glu Gly Phe Arg Leu Lys Gly Arg Ser Ala Ser His Cys
 1700 1705 1710
 Val Leu Ala Gly Met Lys Ala Leu Trp Asn Ser Ser Val Pro Val Cys
 1715 1720 1725
 Glu Gln Ile Phe Cys Pro Asn Pro Pro Ala Ile Leu Asn Gly Arg His
 1730 1735 1740

Thr Gly Thr Pro Phe Gly Asp Ile Pro Tyr Gly Lys Glu Ile Ser Tyr
 1745 1750 1755 1760
 Ala Cys Asp Thr His Pro Asp Arg Gly Met Thr Phe Asn Leu Ile Gly
 1765 1770 1775
 Glu Ser Ser Ile Arg Cys Thr Ser Asp Pro Gln Gly Asn Gly Val Trp
 1780 1785 1790
 Ser Ser Pro Ala Pro Arg Cys Glu Leu Ser Val Pro Ala Ala Cys Pro
 1795 1800 1805
 His Pro Pro Lys Ile Gln Asn Gly His Tyr Ile Gly Gly His Val Ser
 1810 1815 1820
 Leu Tyr Leu Pro Gly Met Thr Ile Ser Tyr Thr Cys Asp Pro Gly Tyr
 1825 1830 1835 1840
 Leu Leu Val Gly Lys Gly Phe Ile Phe Cys Thr Asp Gln Gly Ile Trp
 1845 1850 1855
 Ser Gln Leu Asp His Tyr Cys Lys Glu Val Asn Cys Ser Phe Pro Leu
 1860 1865 1870
 Phe Met Asn Gly Ile Ser Lys Glu Leu Glu Met Lys Lys Val Tyr His
 1875 1880 1885
 Tyr Gly Asp Tyr Val Thr Leu Lys Cys Glu Asp Gly Tyr Thr Leu Glu
 1890 1895 1900
 Gly Ser Pro Trp Ser Gln Cys Gln Ala Asp Asp Arg Trp Asp Pro Pro
 1905 1910 1915 1920
 Leu Ala Lys Cys Thr Ser Arg Ala His Cys Cys Asp Gly Pro Lys Lys
 1925 1930 1935
 Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
 1940 1945

<210> 11
 <211> 215
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (198)..(199)
 <223> Residues 1-198 are a first polypeptide chain and
 residues 199-215 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (199)
 <223> The cysteine at position 199 is linked to a
 NHCOCH3 group

<220>
 <221> UNSURE
 <222> (215)
 <223> The C-terminal lysine is is linked to an
 N-[Myristoyl]-NH2 group

<220>
 <223> Description of Artificial Sequence:
 [SCR1-3]-Cys-S-S-[MSWP-2]

<400> 11

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys
 195 200 205

Ser Pro Ser Lys Ser Ser Lys
 210 215

<210> 12
 <211> 213
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (198)..(199)
 <223> Residues 1-198 are a first polypeptide chain and
 residues 199-213 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 198 and 199

<220>
 <221> UNSURE
 <222> (199)
 <223> The cysteine at position 199 is linked to a CONH2
 group

<220>
 <221> UNSURE
 <222> (213)
 <223> The C-terminal serine is linked to an
 NH-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence:
 [SCR1-3]-Cys-S-S-[MSWP-3]

<400> 12
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15
 Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30
 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45
 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60
 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Cys Cys Lys Thr Lys Ser Lys Lys Lys Lys
195 200 205

Lys Gly Asp Lys Ser
210

<210> 13
<211> 214
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (198)..(199)
<223> Residues 1-198 are a first polypeptide chain and
residues 199-214 are a second polypeptide chain
linked by a disulphide bond formed between the
cysteines at positions 198 and 199

<220>
<221> UNSURE
<222> (199)
<223> The cysteine at position 199 is linked to an
NHCOCH3 group

<220>
<221> UNSURE
<222> (214)
<223> The C-terminal valine is linked to an -NH(CH2)9CH3
group.

<220>
<223> Description of Artificial Sequence:
[SCR1-3]-Cys-S-S-[TCPT-1]

<400> 13
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45
Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60
Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80
Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95
Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110
Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Cys Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg
195 200 205

Ile Leu Leu Leu Lys Val
210

<210> 14
<211> 209
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: SCR1-3 with
the C-terminal amino acids N195 and K196 replaced
by a 14 amino acid peptide.

<400> 14
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Thr Asn Ala Asn Lys Ser Leu Ser Ser Ile Ser Cys Gln
195 200 205

Thr

<210> 15
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used to generate a novel
restriction site and a C-terminal cysteine in
plasmid pBC04-29

<400> 15
ctggagcggg cccgcaccgc agtgcacatcat cccgaacaaa tgctaataaa agc 53

<210> 16
<211> 53
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used to generate a novel
restriction site and C-terminal cysteine residue
in plasmid pBC04-29

<400> 16
gcttttatta gcatttggtc gggatgatgc actgcgggtgc gggcccgcctc cag 53

<210> 17
<211> 224
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)..(209)
<223> Positions 1-209 are a first polypeptide chain
which is linked to a second polypeptide chain
(positions 210-224) by a disulphide linkage
between the cysteines at positions 207 and 210.

<220>
<221> UNSURE
<222> (210)
<223> The cysteine at position 210 is linked to a -CONH2
group

<220>

<221> UNSURE

<222> (224)

<223> The glycine at position 224 is linked to an
-NH-[Myristoyl] group

<220>

<223> Description of Artificial Sequence:

[SCR1-3(delN195-K196)]TNANKSLSSISC-(-S-S-[MSWP-1])

QT

<400> 17

Met	Gln	Cys	Asn	Ala	Pro	Glu	Trp	Leu	Pro	Phe	Ala	Arg	Pro	Thr	Asn	
1				5				10						15		
Leu	Thr	Asp	Glu	Phe	Glu	Phe	Pro	Ile	Gly	Thr	Tyr	Leu	Asn	Tyr	Glu	
		20						25					30			
Cys	Arg	Pro	Gly	Tyr	Ser	Gly	Arg	Pro	Phe	Ser	Ile	Ile	Cys	Leu	Lys	
		35					40						45			
Asn	Ser	Val	Trp	Thr	Gly	Ala	Lys	Asp	Arg	Cys	Arg	Arg	Lys	Ser	Cys	
	50					55					60					
Arg	Asn	Pro	Pro	Asp	Pro	Val	Asn	Gly	Met	Val	His	Val	Ile	Lys	Gly	
65					70					75					80	
Ile	Gln	Phe	Gly	Ser	Gln	Ile	Lys	Tyr	Ser	Cys	Thr	Lys	Gly	Tyr	Arg	
			85					90						95		
Leu	Ile	Gly	Ser	Ser	Ser	Ala	Thr	Cys	Ile	Ile	Ser	Gly	Asp	Thr	Val	
			100					105					110			
Ile	Trp	Asp	Asn	Glu	Thr	Pro	Ile	Cys	Asp	Arg	Ile	Pro	Cys	Gly	Leu	
		115					120					125				
Pro	Pro	Thr	Ile	Thr	Asn	Gly	Asp	Phe	Ile	Ser	Thr	Asn	Arg	Glu	Asn	
	130					135						140				
Phe	His	Tyr	Gly	Ser	Val	Val	Thr	Tyr	Arg	Cys	Asn	Pro	Gly	Ser	Gly	
145					150					155					160	
Gly	Arg	Lys	Val	Phe	Glu	Leu	Val	Gly	Glu	Pro	Ser	Ile	Tyr	Cys	Thr	
			165					170						175		
Ser	Asn	Asp	Asp	Gln	Val	Gly	Ile	Trp	Ser	Gly	Pro	Ala	Pro	Gln	Cys	
		180						185					190			
Ile	Ile	Pro	Thr	Asn	Ala	Asn	Lys	Ser	Leu	Ser	Ser	Ile	Ser	Cys	Gln	
		195					200						205			
Thr	Cys	Asp	Gly	Pro	Lys	Lys	Lys	Lys	Lys	Lys	Ser	Lys	Ser	Ser	Gly	
210						215					220					

<210> 18

<211> 17

<212> PRT

<213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (17)
 <223> The C-terminal lysine is linked to an -NH2 group

<220>
 <223> Description of Artificial Sequence: Peptide used
 to generate SEQ ID NO.28

<400> 18
 Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser
 1 5 10 15
 Lys

<210> 19
 <211> 15
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide used
 to generate SEQ ID NO.29

<400> 19
 Ser Lys Asp Gly Lys Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys
 1 5 10 15

<210> 20
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Peptide used
 to generate SEQ ID NO.30

<400> 20
 Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
 1 5 10 15

<210> 21
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal glycine is linked to an
 N-[Myristoyl]- group

<220>
 <221> UNSURE
 <222> (17)
 <223> The C-terminal cysteine is linked to
 -S-S-[4-butyrimino]-N-epsilon(Lys) [Streptokinase]

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal cysteine is linked to an -NH₂ group

<220>

<223> Description of Artificial Sequence: Conjugate of Streptokinase and MSWP-1

<400> 21

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 22

<211> 527

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (478)

<223> Serine 478 is modified to:

O-4-CO-benzyl-NH(CH₂)₂NHCO(CH₂)₂-S-S-{Cys(-CONH₂)-
Asp-Gly-Pro-Lys-Lys-Lys-Lys-Lys-Lys-Ser-Pro-Ser-Ly
s-Ser-Ser-Gly}-~NH-[Myristoyl]

<220>

<223> Description of Artificial Sequence: Reversible linkage of MSWP-1 to the active centre of Human Tissue-type Plasminogen Activator

<400> 22

Ser Tyr Gln Val Ile Cys Arg Asp Glu Lys Thr Gln Met Ile Tyr Gln
1 5 10 15

Gln His Gln Ser Trp Leu Arg Pro Val Leu Arg Ser Asn Arg Val Glu
20 25 30

Tyr Cys Trp Cys Asn Ser Gly Arg Ala Gln Cys His Ser Val Pro Val
35 40 45

Lys Ser Cys Ser Glu Pro Arg Cys Phe Asn Gly Gly Thr Cys Gln Gln
50 55 60

Ala Leu Tyr Phe Ser Asp Phe Val Cys Gln Cys Pro Glu Gly Phe Ala
65 70 75 80

Gly Lys Cys Cys Glu Ile Asp Thr Arg Ala Thr Cys Tyr Glu Asp Gln
85 90 95

Gly Ile Ser Tyr Arg Gly Thr Trp Ser Thr Ala Glu Ser Gly Ala Glu
100 105 110

Cys Thr Asn Trp Asn Ser Ser Ala Leu Ala Gln Lys Pro Tyr Ser Gly
115 120 125

Arg Arg Pro Asp Ala Ile Arg Leu Gly Leu Gly Asn His Asn Tyr Cys
 130 135 140
 Arg Asn Pro Asp Arg Asp Ser Lys Pro Trp Cys Tyr Val Phe Lys Ala
 145 150 155 160
 Gly Lys Tyr Ser Ser Glu Phe Cys Ser Thr Pro Ala Cys Ser Glu Gly
 165 170 175
 Asn Ser Asp Cys Tyr Phe Gly Asn Gly Ser Ala Tyr Arg Gly Thr His
 180 185 190
 Ser Leu Thr Glu Ser Gly Ala Ser Cys Leu Pro Trp Asn Ser Met Ile
 195 200 205
 Leu Ile Gly Lys Val Tyr Thr Ala Gln Asn Pro Ser Ala Gln Ala Leu
 210 215 220
 Gly Leu Gly Lys His Asn Tyr Cys Arg Asn Pro Asp Gly Asp Ala Lys
 225 230 235 240
 Pro Trp Cys His Val Leu Lys Asn Arg Arg Leu Thr Trp Glu Tyr Cys
 245 250 255
 Asp Val Pro Ser Cys Ser Thr Cys Gly Leu Arg Gln Tyr Ser Gln Pro
 260 265 270
 Gln Phe Arg Ile Lys Gly Gly Leu Phe Ala Asp Ile Ala Ser His Pro
 275 280 285
 Trp Gln Ala Ala Ile Phe Ala Lys His Arg Arg Ser Pro Gly Glu Arg
 290 295 300
 Phe Leu Cys Gly Gly Ile Leu Ile Ser Ser Cys Trp Ile Leu Ser Ala
 305 310 315 320
 Ala His Cys Phe Gln Glu Arg Phe Pro Pro His His Leu Thr Val Ile
 325 330 335
 Leu Gly Arg Thr Tyr Arg Val Val Pro Gly Glu Glu Glu Gln Lys Phe
 340 345 350
 Glu Val Glu Lys Tyr Ile Val His Lys Glu Phe Asp Asp Asp Thr Tyr
 355 360 365
 Asp Asn Asp Ile Ala Leu Leu Gln Leu Lys Ser Asp Ser Ser Arg Cys
 370 375 380
 Ala Gln Glu Ser Ser Val Val Arg Thr Val Cys Leu Pro Pro Ala Asp
 385 390 395 400
 Leu Gln Leu Pro Asp Trp Thr Glu Cys Glu Leu Ser Gly Tyr Gly Lys
 405 410 415
 His Glu Ala Leu Ser Pro Phe Tyr Ser Glu Arg Leu Lys Glu Ala His
 420 425 430
 Val Arg Leu Tyr Pro Ser Ser Arg Cys Thr Ser Gln His Leu Leu Asn
 435 440 445

Arg Thr Val Thr Asp Asn Met Leu Cys Ala Gly Asp Thr Arg Ser Gly
450 455 460

Gly Pro Gln Ala Asn Leu His Asp Ala Cys Gln Gly Asp Ser Gly Gly
465 470 475 480

Pro Leu Val Cys Leu Asn Asp Gly Arg Met Thr Leu Val Gly Ile Ile
485 490 495

Ser Trp Gly Leu Gly Cys Gly Gln Lys Asp Val Pro Gly Val Tyr Thr
500 505 510

Lys Val Thr Asn Tyr Leu Asp Trp Ile Arg Asp Asn Met Arg Pro
515 520 525

<210> 23

<211> 211

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an
additional 14 amino acid residues at the
C-terminus

<400> 23

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe
195 200 205

Ser Ser Cys
210

<210> 24
<211> 228
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (211)..(212)
<223> Residues 1-211 are a first polypeptide chain and
residues 212-228 are a second polypeptide chain
linked by a disulphide bond formed between the
cysteines at positions 211 and 212

<220>
<221> UNSURE
<222> (228)
<223> The C-terminal glycine is linked to an
-NH-[Myristoyl] group

<220>
<223> Description of Artificial Sequence: SCR1-3 with an
additional C-terminal 14 amino acid residues
reacted with MSWP-1

<400> 24
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30
Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45
Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60
Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80
Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95
Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110
Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125
Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190

Ile Ile Pro Asn Lys Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe
 195 200 205

Ser Ser Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser
 210 215 220

Lys Ser Ser Gly
 225

<210> 25
 <211> 72
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide used with the oligonucleotide of
 SEQ ID NO. 26 and plasmid pBC04-29 to generate
 pBC04-31

<400> 25
 cgcaccgcag tgcacatcc cgaacaaaga tggcccgagc gaaattctgc gtggcgattt 60
 tagcagctgc ta 72

<210> 26
 <211> 80
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence:
 Oligonucleotide used with oligonucleotide of SEQ
 ID NO. 25 and plasmid pBC04-29 to generate plasmid
 pBC04-31

<400> 26
 acgttagcag ctgctaaaat cgccacgcag aatttcgctc gggccatctt tgttcgggat 60
 gatgcactgc ggtgcgggcc 80

<210> 27
 <211> 17
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal glycine is linked to an
 N-[Myristoyl]- group

<220>

<223> Description of Artificial Sequence:
Myristoyl/Electrostatic Switch Peptide Reagent 1
(MSWP-1)

<220>

<221> UNSURE

<222> (17)

<223> The cysteine at position 17 is (S-
2-Thiopyridyl)Cys-NH2

<400> 27

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (1)

<223> The N-terminal Cys is
N-acetyl-(S-2-thiopyridyl)Cys-

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal lysine is
-(epsilonN-(Myristoyl))Lys-NH2

<220>

<223> Description of Artificial Sequence:
Myristoyl/Electrostatic Switch Peptide Reagent 2
(MSWP-2)

<400> 28

Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser
1 5 10 15

Lys

<210> 29

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (1)

<223> The N-terminal serine is N-(Myristoyl)-Ser-

<220>
 <221> UNSURE
 <222> (15)
 <223> The C-terminal cysteine is
 -(S-2-Thiopyrolyl)Cys-NH2

<220>
 <223> Description of Artificial Sequence:
 Myristoyl/Electrostatic Switch Peptide Reagent 3
 (MSWP-3)

<400> 29
 Ser Lys Asp Gly Lys Lys Lys Lys Lys Ser Lys Thr Lys Cys
 1 5 10 15

<210> 30
 <211> 16
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (1)
 <223> The N-terminal cysteine is
 N-acetyl-(S-2-thiopyridyl)Cys-

<220>
 <221> UNSURE
 <222> (16)
 <223> The C-terminal valine is -Val-NH(CH2)9CH3

<220>
 <223> Description of Artificial Sequence: T-cell
 targetting peptide reagent 1 (TCTP-1)

<400> 30
 Cys Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
 1 5 10 15

<210> 31
 <211> 214
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (214)
 <223> The C-terminal cysteine is
 -Cys-S-S-(CH2)2-CONH-(CH2)12CH3

<220>
 <223> Description of Artificial Sequence: [SCR1-3/switch
 fusion]disulphide linked to [MAET]

<400> 31
 Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
 1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
 20 25 30
 Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45
 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60
 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro
 195 200 205
 Ser Lys Ser Ser Gly Cys
 210

<210> 32

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<221> UNSURE

<222> (1)

<223> The N-terminal Glycine is N-(Myristoyl)-Gly-

<220>

<221> UNSURE

<222> (17)

<223> The C-terminal cysteine is linked to an amino group and is also linked via a disulphide bond to -[4-butyrimino]-N-epsilon(Lys)[Rabbit anti-(human erythrocyte membrane)] antibody].

<220>

<223> Description of Artificial Sequence: Rabbit anti-(human erythrocyte membrane)

antibody-[MSWP-1] conjugate.

<400> 32

Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 33

<211> 214

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: SCR1-3 with an
additional C-terminal 18 amino acids

<400> 33

Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15

Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
35 40 45

Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
50 55 60

Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
65 70 75 80

Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
85 90 95

Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
100 105 110

Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
115 120 125

Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
130 135 140

Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
145 150 155 160

Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
165 170 175

Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
180 185 190

Ile Ile Pro Asn Lys Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu
195 200 205

Leu Leu Lys Val Gly Cys
210

<210> 34
<211> 84
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used with oligonucleotide of SEQ
ID NO.35 and plasmid pBC04-29 to generate plasmid
pBC04-34

<400> 34
cgcaccgcag tgcacatcc cgaacaaagc ggcgccagc gtgattggct tccgtattct 60
gctgctgaaa gtggcgggct gcta 84

<210> 35
<211> 92
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence:
Oligonucleotide used with the oligonucleotide of
SEQ ID NO. 34 and plasmid pBC04-29 to generate
plasmid pBC04-34

<400> 35
agcttagcag cccgccactt tcagcagcag aatacggaag ccaatcacgc tgggcgcgcg 60
ttgttcggg atgatgcact gcggtgcggg cc 92

<210> 36
<211> 231
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (214)..(215)
<223> Residues 1-214 are a first polypeptide chain and
residues 215-231 are a second polypeptide chain
linked by a disulphide bond formed between the
cysteines at positions 214 and 215

<220>
<221> UNSURE
<222> (231)
<223> The C-terminal glycine is -Gly-NH-[Myristoyl]

<220>
<223> Description of Artificial Sequence: [SCR1-3] with
an additional 18 C-terminal amino acid residues
linked via a disulphide bond to MSWP-1

<400> 36
Met Gln Cys Asn Ala Pro Glu Trp Leu Pro Phe Ala Arg Pro Thr Asn
1 5 10 15
Leu Thr Asp Glu Phe Glu Phe Pro Ile Gly Thr Tyr Leu Asn Tyr Glu
20 25 30

Cys Arg Pro Gly Tyr Ser Gly Arg Pro Phe Ser Ile Ile Cys Leu Lys
 35 40 45
 Asn Ser Val Trp Thr Gly Ala Lys Asp Arg Cys Arg Arg Lys Ser Cys
 50 55 60
 Arg Asn Pro Pro Asp Pro Val Asn Gly Met Val His Val Ile Lys Gly
 65 70 75 80
 Ile Gln Phe Gly Ser Gln Ile Lys Tyr Ser Cys Thr Lys Gly Tyr Arg
 85 90 95
 Leu Ile Gly Ser Ser Ser Ala Thr Cys Ile Ile Ser Gly Asp Thr Val
 100 105 110
 Ile Trp Asp Asn Glu Thr Pro Ile Cys Asp Arg Ile Pro Cys Gly Leu
 115 120 125
 Pro Pro Thr Ile Thr Asn Gly Asp Phe Ile Ser Thr Asn Arg Glu Asn
 130 135 140
 Phe His Tyr Gly Ser Val Val Thr Tyr Arg Cys Asn Pro Gly Ser Gly
 145 150 155 160
 Gly Arg Lys Val Phe Glu Leu Val Gly Glu Pro Ser Ile Tyr Cys Thr
 165 170 175
 Ser Asn Asp Asp Gln Val Gly Ile Trp Ser Gly Pro Ala Pro Gln Cys
 180 185 190
 Ile Ile Pro Asn Lys Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu
 195 200 205
 Leu Leu Lys Val Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys
 210 215 220
 Ser Pro Ser Lys Ser Ser Gly
 225 230

<210> 37
 <211> 77
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Protein APT631

<400> 37
 Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
 1 5 10 15
 Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
 20 25 30
 Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
 35 40 45
 Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
 50 55 60

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn
65 70 75

<210> 38
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (1)
<223> The N-terminal glycine is linked to an
N-[Myristoyl]- group

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal cysteine is linked to
-2-thiopyridyl

<220>
<221> UNSURE
<222> (17)
<223> The C-terminal cysteine is linked to an -NH2 group

<220>
<223> Description of Artificial Sequence: Protein APT542

<400> 38
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

Cys

<210> 39
<211> 70
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Protein APT634

<400> 39
Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Ala Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn
65 70

<210> 40
<211> 82
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Protein APT2060

<400> 40

Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
1 5 10 15

Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
50 55 60

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly Thr
65 70 75 80

Ser Cys

<210> 41
<211> 83
<212> PRT
<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Protein APT635

<400> 41

Met Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
1 5 10 15

Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala
20 25 30

Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe
35 40 45

Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys
50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly
65 70 75 80

Thr Ser Cys

<210> 42
 <211> 71
 <212> PRT
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Protein APT2061

<400> 42

Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
 1 5 10 15

Val Ala Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
 20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
 35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
 50 55 60

Lys Lys Asp Leu Cys Asn Cys
 65 70

<210> 43
 <211> 99
 <212> PRT
 <213> Artificial Sequence

<220>

<221> UNSURE

<222> (82)..(83)

<223> Residues 1-82 are a first polypeptide chain and
 residues 83-99 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 82 and 83

<220>

<221> UNSURE

<222> (99)

<223> The C-terminal glycine is linked to an
 NH-[Myristoyl] group

<220>

<223> Description of Artificial Sequence: Protein APT2062

<400> 43

Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
 1 5 10 15

Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
 20 25 30

Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
 35 40 45

Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
 50 55 60

Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly Thr
65 70 75 80

Ser Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys
85 90 95

Ser Ser Gly

<210> 44
<211> 100
<212> PRT
<213> Artificial Sequence

<220>
<221> UNSURE
<222> (83)..(84)
<223> Residues 1-83 are a first polypeptide chain and
residues 84-100 are a second polypeptide chain
linked by a disulphide bond formed between the
cysteines at positions 83 and 84

<220>
<221> UNSURE
<222> (100)
<223> The C-terminal glycine is linked to an
NH-[Myristoyl] group

<220>
<223> Description of Artificial Sequence: Protein APT2063

<400> 44
Met Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr
1 5 10 15

Ala Val Asn Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala
20 25 30

Gly Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe
35 40 45

Asn Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys
50 55 60

Cys Lys Lys Asp Leu Cys Asn Phe Asn Glu Gln Leu Glu Asn Gly Gly
65 70 75 80

Thr Ser Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser
85 90 95

Lys Ser Ser Gly
100

<210> 45
<211> 88
<212> PRT
<213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (71)..(72)
 <223> Residues 1-71 are a first polypeptide chain and
 residues 72-88 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 71 and 72

<220>
 <221> UNSURE
 <222> (88)
 <223> The C-terminal glycine is linked to an
 NH-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence: Protein APT2065

<400> 45
 Leu Gln Cys Tyr Asn Cys Pro Asn Pro Thr Ala Asp Cys Lys Thr Ala
 1 5 10 15
 Val Ala Cys Ser Ser Asp Phe Asp Ala Cys Leu Ile Thr Lys Ala Gly
 20 25 30
 Leu Gln Val Tyr Asn Lys Cys Trp Lys Phe Glu His Cys Asn Phe Asn
 35 40 45
 Asp Val Thr Thr Arg Leu Arg Glu Asn Glu Leu Thr Tyr Tyr Cys Cys
 50 55 60
 Lys Lys Asp Leu Cys Asn Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys
 65 70 75 80
 Lys Ser Pro Ser Lys Ser Ser Gly
 85

<210> 46
 <211> 211
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Protein APT2057

<400> 46
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala
 20 25 30
 Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr
 35 40 45
 Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu
 50 55 60
 Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val
 65 70 75 80

Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn
 85 90 95
 Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser
 100 105 110
 Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe
 115 120 125
 Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu
 130 135 140
 Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile
 145 150 155 160
 Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr
 165 170 175
 Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys
 180 185 190
 Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys
 195 200 205
 Arg Gly Cys
 210

<210> 47
 <211> 274
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> Description of Artificial Sequence: Protein APT2058

<400> 47
 Met Gly Ser Ser His His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Gln Asp Cys Gly Leu Pro Pro Asp Val Pro Asn
 20 25 30
 Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val
 35 40 45
 Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys
 50 55 60
 Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu
 65 70 75 80
 Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser
 85 90 95
 Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val
 100 105 110
 Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser
 115 120 125

Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu
 130 135 140
 Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly
 145 150 155 160
 Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe
 165 170 175
 Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys
 180 185 190
 Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys
 195 200 205
 Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile
 210 215 220
 Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala
 225 230 235 240
 Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr
 245 250 255
 Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg
 260 265 270

Gly Cys

<210> 48
 <211> 291
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (274) .. (275)
 <223> Residues 1-274 are a first polypeptide chain and
 residues 275-291 are a second polypeptide chain
 linked by a disulphide bond formed between the
 cysteines at positions 274 and 275

<220>
 <221> UNSURE
 <222> (291)
 <223> The C-terminal glycine is linked to an
 NH-[Myristoyl] group

<220>
 <223> Description of Artificial Sequence: Protein APT2160

<400> 48
 Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1 5 10 15
 Arg Gly Ser His Met Gln Asp Cys Gly Leu Pro Pro Asp Val Pro Asn
 20 25 30

Ala Gln Pro Ala Leu Glu Gly Arg Thr Ser Phe Pro Glu Asp Thr Val
 35 40 45
 Ile Thr Tyr Lys Cys Glu Glu Ser Phe Val Lys Ile Pro Gly Glu Lys
 50 55 60
 Asp Ser Val Ile Cys Leu Lys Gly Ser Gln Trp Ser Asp Ile Glu Glu
 65 70 75 80
 Phe Cys Asn Arg Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala Ser
 85 90 95
 Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr Val
 100 105 110
 Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu Ser
 115 120 125
 Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val Glu
 130 135 140
 Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn Gly
 145 150 155 160
 Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser Phe
 165 170 175
 Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe Cys
 180 185 190
 Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu Cys
 195 200 205
 Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile Ile
 210 215 220
 Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr Ala
 225 230 235 240
 Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys Thr
 245 250 255
 Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys Arg
 260 265 270
 Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Ser Pro Ser Lys
 275 280 285
 Ser Ser Gly
 290

<210> 49
 <211> 228
 <212> PRT
 <213> Artificial Sequence

<220>
 <221> UNSURE
 <222> (211)..(212)
 <223> Residues 1-211 are a first polypeptide chain and

residues 212-228 are a second polypeptide chain
linked by a disulphide bond formed between the
cysteines at positions 211 and 212

<220>

<221> UNSURE

<222> (228)

<223> The C-terminal glycine is linked to an
NH-[Myristoyl] group

<220>

<223> Description of Artificial Sequence: Protein APT2184

<400> 49

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Met Gly Ser Ser His His His His His Ser Ser Gly Leu Val Pro
 1             5             10             15

Arg Gly Ser His Met Ser Cys Glu Val Pro Thr Arg Leu Asn Ser Ala
          20             25             30

Ser Leu Lys Gln Pro Tyr Ile Thr Gln Asn Tyr Phe Pro Val Gly Thr
          35             40             45

Val Val Glu Tyr Glu Cys Arg Pro Gly Tyr Arg Arg Glu Pro Ser Leu
          50             55             60

Ser Pro Lys Leu Thr Cys Leu Gln Asn Leu Lys Trp Ser Thr Ala Val
          65             70             75             80

Glu Phe Cys Lys Lys Lys Ser Cys Pro Asn Pro Gly Glu Ile Arg Asn
          85             90             95

Gly Gln Ile Asp Val Pro Gly Gly Ile Leu Phe Gly Ala Thr Ile Ser
          100            105            110

Phe Ser Cys Asn Thr Gly Tyr Lys Leu Phe Gly Ser Thr Ser Ser Phe
          115            120            125

Cys Leu Ile Ser Gly Ser Ser Val Gln Trp Ser Asp Pro Leu Pro Glu
          130            135            140

Cys Arg Glu Ile Tyr Cys Pro Ala Pro Pro Gln Ile Asp Asn Gly Ile
          145            150            155            160

Ile Gln Gly Glu Arg Asp His Tyr Gly Tyr Arg Gln Ser Val Thr Tyr
          165            170            175

Ala Cys Asn Lys Gly Phe Thr Met Ile Gly Glu His Ser Ile Tyr Cys
          180            185            190

Thr Val Asn Asn Asp Glu Gly Glu Trp Ser Gly Pro Pro Pro Glu Cys
          195            200            205

Arg Gly Cys Cys Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser
          210            215            220

Lys Ser Ser Gly
          225

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<210> 50
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 50
Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
1 5 10 15

<210> 51
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 51
Gly Ser Ser Lys Ser Pro Ser Lys Lys Lys Lys Lys Lys Pro Gly Asp
1 5 10 15

<210> 52
<211> 20
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 52
Ser Pro Ser Asn Glu Thr Pro Lys Lys Lys Lys Lys Arg Phe Ser Phe
1 5 10 15

Lys Lys Ser Gly
20

<210> 53
<211> 16
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 53
Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Lys
1 5 10 15

<210> 54
<211> 14
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 54
Ser Lys Asp Gly Lys Lys Lys Lys Lys Lys Ser Lys Thr Lys
1 5 10

<210> 55
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 55
Gly Arg Gly Asp Ser Pro
1 5

<210> 56
<211> 13
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 56
Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser
1 5 10

<210> 57
<211> 17
<212> PRT
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: illustrative amino
acid sequence

<400> 57
Gly Asn Glu Gln Ser Phe Arg Val Asp Leu Arg Thr Leu Leu Arg Tyr
1 5 10 15

Ala

<210> 58
<211> 9
<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 58

Gly Phe Arg Ile Leu Leu Leu Lys Val
1 5

<210> 59

<211> 15

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 59

Ser Ala Ala Pro Ser Ser Gly Phe Arg Ile Leu Leu Leu Lys Val
1 5 10 15

<210> 60

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 60

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
1 5 10 15

Gly

<210> 61

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 61

Asp Gly Pro Lys Lys Lys Lys Lys Lys Ser Pro Ser Lys Ser Ser Gly
1 5 10 15

Cys

<210> 62

<211> 18

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 62

Ala Ala Pro Ser Val Ile Gly Phe Arg Ile Leu Leu Leu Lys Val Ala
1 5 10 15

Gly Cys

<210> 63

<211> 14

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative amino acid sequence

<400> 63

Asp Gly Pro Ser Glu Ile Leu Arg Gly Asp Phe Ser Ser Cys
1 5 10

<210> 64

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: illustrative DNA oligonucleotide

<400> 64

cctctggcca aatgtacctc tcgtgcacat tgctga

36

<210> 65

<211> 20

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Amino acid leader sequence

<400> 65

Met Gly Ser Ser His His His His Ser Ser Gly Leu Val Pro
1 5 10 15

Arg Gly Ser His
20

<210> 66
<211> 31
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Primer DAF-R

<400> 66
ggaattctaa gtcagcaagc ccatggttac t

31

<210> 67
<211> 25
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Oligonucleotide
DAF-F

<400> 67
gcatatgacc gtcgcgcggc cgagc

25